



Rec'd PCT/PTO 04 OCT 2005

Sequence Listing

<110> Sode,
<120> Glucose Dehydrogenase
<130> 3691-0114PUS1
<140> US 10/520,126
<141> 2005-01-03
<150> PCT/JP03/08418
<151> 2002-07-02
<150> JP 2003-71760
<151> 2003-03-17
<150> JP 2002-196177
<151> 2002-07-04
<160> 19
<170> PatentIn version 3.3
<210> 1
<211> 454
<212> PRT
<213> Acinetobacter calcoaceticus

<400> 1
Asp Val Pro Leu Thr Pro Ser Gln Phe Ala Lys Ala Lys Ser Glu Asn
1 5 10 15
Phe Asp Lys Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu
20 25 30
Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly
35 40 45
Lys Ile Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe
50 55 60
Gln Val Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu
65 70 75 80
Gly Phe Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Ile
85 90 95
Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
100 105 110
Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ser Thr Asp Thr Leu
115 120 125
Glu Lys Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His
130 135 140
Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
145 150 155 160
Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
165 170 175
Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Gly Lys Asp Tyr
180 185 190
His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Ile
195 200 205
Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr

210		215		220
Leu Gly His Arg Asn	Pro Gln Gly Leu Ala Phe	Thr Pro Asn Gly Lys		
225	230	235	240	
Leu Leu Gln Ser Glu	Gln Gly Pro Asn Ser Asp	Asp Glu Ile Asn Leu		
	245	250	255	
Ile Val Lys Gly Gly	Asn Tyr Gly Trp Pro Asn	Val Ala Gly Tyr Lys		
	260	265	270	
Asp Asp Ser Gly Tyr	Ala Tyr Ala Asn Tyr Ser	Ala Ala Ala Asn Lys		
	275	280	285	
Ser Ile Lys Asp Leu	Ala Gln Asn Gly Val Lys	Val Ala Ala Gly Val		
	290	295	300	
Pro Val Thr Lys Glu	Ser Glu Trp Thr Gly Lys	Asn Phe Val Pro Pro		
305	310	315	320	
Leu Lys Thr Leu Tyr	Thr Val Gln Asp Thr Tyr	Asn Tyr Asn Asp Pro		
	325	330	335	
Thr Cys Gly Glu Met	Thr Tyr Ile Cys Trp Pro	Thr Val Ala Pro Ser		
	340	345	350	
Ser Ala Tyr Val Tyr	Lys Gly Gly Lys Lys Ala	Ile Thr Gly Trp Glu		
	355	360	365	
Asn Thr Leu Leu Val	Pro Ser Leu Lys Arg Gly	Val Ile Phe Arg Ile		
	370	375	380	
Lys Leu Asp Pro Thr	Tyr Ser Thr Thr Tyr Asp	Asp Ala Val Pro Met		
385	390	395	400	
Phe Lys Ser Asn Asn	Arg Tyr Arg Asp Val Ile	Ala Ser Pro Asp Gly		
	405	410	415	
Asn Val Leu Tyr Val	Leu Thr Asp Thr Ala Gly	Asn Val Gln Lys Asp		
	420	425	430	
Asp Gly Ser Val Thr	Asn Thr Leu Glu Asn Pro	Gly Ser Leu Ile Lys		
	435	440	445	
Phe Thr Tyr Lys Ala	Lys			
450				

<210> 2
 <211> 1612
 <212> DNA
 <213> Acinetobacter calcoaceticus

<400> 2
 agctactttt atgcaacaga gccttttcaga aatttagatt ttaatagatt cgttattcat 60
 cataatacaa atcatataga gaactcgtac aaacccttta ttagagggttt aaaaattctc 120
 ggaaaatttt gacaatttat aagggtggaca catgaataaa catttattgg ctaaaattgc 180
 tttattaagc gctgttcagc tagttacact ctcagcattt gctgatgttc ctctaactcc 240
 atctcaattt gctaaagcga aatcagagaa ctttgacaag aaagttattc tatctaattc 300
 aaataagccg catgctttgt tatggggacc agataatcaa atttggttaa ctgagcgagc 360
 aacaggtaag attctaagag ttaatccaga gtcgggtagt gtaaaaacag tttttcaggt 420
 accagagatt gtcaatgatg ctgatgggca gaatgggttta ttaggttttg ccttccatcc 480
 tgatttttaa aataatcctt atatctatat tttaggtaca tttaaaaatc cgaaatctac 540
 agataaagaa ttaccgaacc aaacgattat tcgtcgttat acctataata aatcaacaga 600
 tacgctcgag aagccagtcg atttattagc aggattacct tcatcaaaag accatcagtc 660
 aggtcgtcct gtcattgggc cagatcaaaa gatttattat acgattgggtg accaagggcg 720
 taaccagctt gcttatttgc tcttgccaaa tcaagcaca catacgccaa ctcaacaaga 780
 actgaatggt aaagactatc acacctatat gggtaaagta ctacgcttaa atcttgatgg 840
 aagtattcca aaggataatc caagttttta cgggggtggt agccatattt atacacttgg 900
 acatcgtaat ccgcagggtc tagcattcac tcctaatggg aaattattgc agtctgaaca 960
 aggcccaaac tctgacgatg aaattaacct cattgtcaaa ggtggcaatt atgggtggcc 1020
 gaatgtagca gggtataaag atgatagtgg ctatgcttat gcaaattatt cagcagcagc 1080

```

caataagtca  attaaggatt  tagctcaaaa  tggagtaaaa  gtagccgcag  gggtcctgt  1140
gacgaaagaa  tctgaatgga  ctggtaaaaa  ctttgtccca  ccattaaaaa  ctttatatac  1200
cgttcaagat  acctacaact  ataacgatcc  aacttggtga  gagatgacct  acatttgctg  1260
gccaacagtt  gcaccgtcat  ctgcctatgt  ctataagggc  ggtaaaaaag  caattactgg  1320
ttgggaaaat  acattattgg  ttccatcttt  aaaacgtggt  gtcattttcc  gtattaagtt  1380
agatccaact  tatagcacta  cttatgatga  cgctgtaccg  atgtttaaga  gcaacaaccg  1440
ttatcgtgat  gtgattgcaa  gtccagatgg  gaatgtctta  tatgtattaa  ctgatactgc  1500
cggaaatgtc  caaaaagatg  atggctcagt  aacaaataca  ttagaaaacc  caggatctct  1560
cattaagttc  acctataagg  ctaagtaata  cagtcgcatt  aaaaaaccga  tc           1612

```

```

<210> 3
<211> 8
<212> PRT
<213> Acinetobacter calcoaceticus

```

```

<220>
<221> misc_feature
<222> (4)..(5)
<223> Xaa can be any amino acid provided that when Xaa at pos. 4 is Gln, then
      Xaa at pos. 5 is not Leu

```

```

<400> 3
Gly Arg Asn Xaa Xaa Ala Tyr Leu
1           5

```

```

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> synthetic primer for point mutation

```

```

<400> 4
ataagcaagc gggttacgcc c 21

```

```

<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> synthetic primer for point mutation

```

```

<400> 5
caaataagca agcccgttac gcccttg 27

```

```

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

```

```

<220>

```

<223> synthetic primer for point mutation

<400> 6

caaataagca gcctgggttac g 21

<210> 7

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 7

gaacaaataa gcaccctggt tacgccc 27

<210> 8

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 8

cctgactgat gttcttttga tgaagg 26

<210> 9

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 9

catctttttg gacagttccg gcagtat 27

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 10

caaataagca agcaggttac gcccttg 27

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 11

caaataagca agaaagttac gcccttg 27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 12

caaataagca aggctgttac gcccttg 27

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 13

caaataagca aggttggttac gcccttg 27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 14

caaataagca agatcggttac gcccttg 27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic primer for point mutation

<400> 15

caaataagca agttcggttac gcccttg 27

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer for point mutation

<400> 16
caaataagca agtttggttac gcccttg 27

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer for point mutation

<400> 17
gaacaaataa gccatctggt tacgccc 27

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer for point mutation

<400> 18
gaacaaataa gctttctggt tacgccc 27

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic primer for point mutation

<400> 19
gaacaaataa gccactggt tacgccc 27